

Library Sequence Search History

10/674,516

=> fil reg

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

7.47

41.77

Checked

JSR
6-14-2006

FILE 'REGISTRY' ENTERED AT 15:45:23 ON 24 MAY 2006

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Property values tagged with IC are from the ZIC/VINITI data file provided by InfoChem.

STRUCTURE FILE UPDATES: 23 MAY 2006 HIGHEST RN 885357-09-5

DICTIONARY FILE UPDATES: 23 MAY 2006 HIGHEST RN 885357-09-5

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH January 6, 2006

Please note that search-term pricing does apply when conducting SmartSELECT searches.

*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Structure search iteration limits have been increased. See HELP SLIMITS for details.

REGISTRY includes numerically searchable data for experimental and predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to:

<http://www.cas.org/ONLINE/UG/regprops.html>

=> s cggrwgc/sqsp

L1 2 CGGRWGC/SQSP

=> fil medl,biosis,embase,caplus;s ll

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

28.89

70.66

FILE 'MEDLINE' ENTERED AT 15:45:57 ON 24 MAY 2006

FILE 'BIOSIS' ENTERED AT 15:45:57 ON 24 MAY 2006

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FILE 'EMBASE' ENTERED AT 15:45:57 ON 24 MAY 2006

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FILE 'CAPLUS' ENTERED AT 15:45:57 ON 24 MAY 2006
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L2 0 FILE MEDLINE
L3 0 FILE BIOSIS
L4 0 FILE EMBASE
L5 1 FILE CAPLUS

TOTAL FOR ALL FILES
L6 1 L1

=> d ibib abs hitseq

L6 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:323999 CAPLUS Full-text
DOCUMENT NUMBER: 142:386021
TITLE: Peptide with osteogenic activity, and therapeutic use
INVENTOR(S): Dhanaraj, Sridevi; Gosiewska, Anna; Rezanian, Ali;
Heavner, George A.; Lin, Xuanhan; Yi, Chin-Feng
PATENT ASSIGNEE(S): Ethicon, Inc., USA
SOURCE: PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005032461	A2	20050414	WO 2004-US29649	20040910
WO 2005032461	A3	20050707		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, VZ, VC, VN, YU, ZA, ZM, ZW			
RW:	BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
US 2005187162	A1	20050825	US 2003-674516	20030930
PRIORITY APPLN. INFO.:			US 2003-674516	A 20030930
OTHER SOURCE(S):	MARPAT 142:386021			

AB The invention provides a composition including an isolated or recombinant peptide component that has osteogenic cell proliferative activity. The peptide, which promotes proliferation of osteoblasts, is useful for treatment of fractures, as a filler in deficient sites of bone, for inhibition of decrease in bone substance related to osteoporosis and periodontic diseases, and for prevention of fractures associated with osteoporosis and rheumatoid arthritis. The peptide, or cells that have been genetically engineered to produce the peptide, can be combined with a bone-compatible matrix to facilitate slow release of the peptide to a treatment site and/or provide a structure for developing bone.

IT 849774-60-3

RL: DEV (Device component use); PAC (Pharmacological activity); PRP

(Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(peptide with osteogenic activity, and therapeutic use)
RN 849774-60-3 CAPLUS
CN Glycine, L-cysteinylglycylglycylglycyl-L-arginyl-L-tryptophyl-L-cysteinyl-
(9CI) (CA INDEX NAME)

=> dis his

(FILE 'MEDLINE, BIOSIS, EMBASE, CAPLUS' ENTERED AT 15:44:28 ON 24 MAY
2006)

DEL HIS Y

FILE 'REGISTRY' ENTERED AT 15:45:23 ON 24 MAY 2006

L1 2 S CGGGRWCG/SQSP

FILE 'MEDLINE, BIOSIS, EMBASE, CAPLUS' ENTERED AT 15:45:57 ON 24 MAY 2006

L2 0 FILE MEDLINE

L3 0 FILE BIOSIS

L4 0 FILE EMBASE

L5 1 FILE CAPLUS

TOTAL FOR ALL FILES

L6 1 S L1

=> log y

OM protein - protein search, using sw model

Run on: May 23, 2006, 20:22:49 ; Search time 297 Seconds
 (without alignments)
 24.916 Million cell updates/sec

Title: US-10-674-516B-1
 Perfect score: 58
 Sequence: 1 CGGGRWCG 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	49	84.5	104	2	Q6Z7M0_ORYSA	Q6z7m0 oryza sativ	
2	48	82.8	360	2	Q75IX4_ORYSA	Q75ix4 oryza sativ	
3	47	81.0	172	2	Q2KQ04_ARAHY	Q2kq04 arachis hyp	
4	46	79.3	105	2	Q5Z750_ORYSA	Q5z750 oryza sativ	
5	46	79.3	427	2	Q8H033_ORYSA	Q8h033 oryza sativ	
6	46	79.3	427	2	Q947X5_ORYSA	Q947x5 oryza sativ	
7	45	77.6	273	1	ENV_FLVC1	P21444 feline leuk	
8	45	77.6	273	2	Q9J054_FLV	Q9j054 feline leuk	
9	45	77.6	534	1	ENV_FSVST	P03392 feline sarc	
10	45	77.6	662	1	ENV_FLVLB	P11261 feline leuk	
11	45	77.6	662	1	ENV_FSVGA	P03391 feline sarc	
12	45	77.6	662	2	Q7LYY7_FLV	Q7lyy7 feline leuk	
13	45	77.6	666	2	Q90AE9_FLV	Q90ae9 feline leuk	
14	45	77.6	668	1	ENV_FLVC6	P21443 feline leuk	
15	44	75.9	127	2	Q3WEG8_9ACTO	Q3weg8 frankia sp.	

16	44	75.9	271	2	Q6K7U5_ORYSA	Q6k7u5	oryza sativ
17	44	75.9	759	2	Q8HZM8_HORSE	Q8hzm8	equus cabal
18	44	75.9	1968	2	Q8X0C5_NEUCR	Q8x0c5	neurospora
19	43	74.1	112	2	Q6ZAF3_ORYSA	Q6zaf3	oryza sativ
20	43	74.1	118	2	Q43969_AZOCA	Q43969	azorhizobiu
21	43	74.1	128	2	Q84PQ1_ORYSA	Q84pq1	oryza sativ
22	43	74.1	129	2	Q6AVV1_ORYSA	Q6avv1	oryza sativ
23	43	74.1	138	2	Q6YYU6_ORYSA	Q6yyu6	oryza sativ
24	43	74.1	151	2	Q6IKQ2_DROME	Q6ikq2	drosophila
25	43	74.1	172	2	Q8S1B6_ORYSA	Q8slb6	oryza sativ
26	43	74.1	184	2	Q5VNR6_ORYSA	Q5vnr6	oryza sativ
27	43	74.1	191	2	Q5VNR9_ORYSA	Q5vnr9	oryza sativ
28	43	74.1	262	2	Q9VRS9_DROME	Q9vrs9	drosophila
29	43	74.1	262	2	Q2LZC5_DROPS	Q2lzc5	drosophila
30	43	74.1	266	1	Y1374_METJA	Q58769	methanococc
31	43	74.1	274	2	Q84SS0_ORYSA	Q84ss0	oryza sativ
32	43	74.1	305	2	Q7XD80_ORYSA	Q7xd80	oryza sativ
33	43	74.1	305	2	Q8W384_ORYSA	Q8w384	oryza sativ
34	43	74.1	360	2	Q6K612_ORYSA	Q6k612	oryza sativ
35	43	74.1	404	2	Q3IW01_RHOS4	Q3iw01	rhodobacter
36	43	74.1	500	1	AL1A1_MOUSE	P24549	mus musculu
37	43	74.1	500	1	AL1A1_RAT	P51647	rattus norv
38	43	74.1	500	1	AL1A4_RAT	P13601	rattus norv
39	43	74.1	501	2	O35945_MOUSE	O35945	mus musculu
40	43	74.1	507	2	Q80ZX7_MOUSE	Q80zx7	mus musculu
41	43	74.1	565	2	Q75LV4_ORYSA	Q75lv4	oryza sativ
42	43	74.1	606	1	ABCD4_HUMAN	O14678	homo sapien
43	43	74.1	606	2	Q6IAQ0_HUMAN	Q6iaq0	homo sapien
44	43	74.1	606	2	Q96E75_HUMAN	Q96e75	homo sapien
45	43	74.1	3650	2	Q2SW14_BURTH	Q2sw14	burkholderi

ALIGNMENTS

RESULT 1

Q6Z7M0_ORYSA

ID Q6Z7M0_ORYSA PRELIMINARY; PRT; 104 AA.

AC Q6Z7M0;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Hypothetical protein OJ1233_A01.24.

GN Name=OJ1233_A01.24;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Sasaki T., Matsumoto T., Yamamoto K.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

CC

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CC

DR EMBL; AP004845; BAD15787.1; -; Genomic_DNA.

DR Gramene; Q6Z7M0; -.

KW Hypothetical protein.

SQ SEQUENCE 104 AA; 10293 MW; 60BD09F52EE606D6 CRC64;

Query Match 84.5%; Score 49; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGRWCG 8

||||||

Db 22 GGGRWCG 28

Search completed: May 23, 2006, 20:31:02

Job time : 300 secs

OM protein - protein search, using sw model

Run on: May 23, 2006, 20:26:19 ; Search time 38 Seconds
 (without alignments)
 20.256 Million cell updates/sec

Title: US-10-674-516B-1
 Perfect score: 58
 Sequence: 1 CGGGRWCG 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	49	84.5	185	2	S12205	hypothetical prote
2	45	77.6	273	2	B31479	env polyprotein pr
3	45	77.6	347	2	S40105	gene AGP2beta-2 pr
4	45	77.6	534	1	VCVWSF	env polyprotein -
5	45	77.6	662	1	VCMVLB	env polyprotein -
6	45	77.6	662	1	VCVWGF	env polyprotein -
7	45	77.6	662	2	A25982	env polyprotein -
8	45	77.6	668	1	VCMVFP	env polyprotein pr
9	43	74.1	118	2	S52855	hypothetical prote
10	43	74.1	266	2	E64471	hypothetical prote
11	43	74.1	501	1	A32616	aldehyde dehydroge
12	43	74.1	501	1	JQ1004	aldehyde dehydroge
13	43	74.1	501	2	JC4524	aldehyde dehydroge

14	43	74.1	501	2	JC5553	aldehyde dehydroge
15	43	74.1	606	2	JC5604	ABC-transporting p
16	42	72.4	535	2	S58224	oestrogen receptor
17	41	70.7	550	2	T47158	hypothetical prote
18	41	70.7	951	2	T00017	gene ADAMTS-1 prot
19	40	69.0	241	2	C75329	conserved hypothet
20	40	69.0	461	2	T06268	probable beta-1,3-
21	39.5	68.1	368	2	G96668	protein F1N19.7 [i
22	39	67.2	54	2	A26463	relaxin - spiny do
23	39	67.2	295	2	JC5559	lectin-B - Virgini
24	38	65.5	138	1	I51381	phospholipase A2 (
25	38	65.5	138	1	PSRSB2	phospholipase A2 (
26	38	65.5	138	1	PSRSBT	phospholipase A2 (
27	38	65.5	264	2	B89005	protein T24A6.18 [
28	38	65.5	385	2	T20410	hypothetical prote
29	38	65.5	393	2	T20268	hypothetical prote
30	38	65.5	697	2	T26707	hypothetical prote
31	38	65.5	787	2	T05617	hypothetical prote
32	37	63.8	44	1	RXRKOT	relaxin - sand tig
33	37	63.8	53	2	C82776	hypothetical prote
34	37	63.8	109	2	PL0233	Ig heavy chain V r
35	37	63.8	112	2	PL0232	Ig heavy chain V r
36	37	63.8	124	2	A21761	high-cysteine chor
37	37	63.8	163	2	T33130	hypothetical prote
38	37	63.8	255	2	T34163	hypothetical prote
39	37	63.8	370	2	JC7998	platelet-derived g
40	37	63.8	370	2	JC7591	spinal cord-derive
41	37	63.8	370	2	JC7592	spinal cord-derive
42	37	63.8	377	2	AD2746	zinc metallopeptid
43	37	63.8	387	2	F82692	conserved hypothet
44	37	63.8	405	2	D81918	sodium-translocati
45	37	63.8	405	2	G81184	Na(+)-translocatin

ALIGNMENTS

RESULT 1

S12205

hypothetical protein 1 (rRNA external transcribed spacer) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1993

C;Accession: S12205

R;Oberbaeumer, I.

submitted to MIPS, January 1991

A;Reference number: S12205

A;Accession: S12205

A;Molecule type: mRNA

A;Residues: 1-185 <OBE>

A;Cross-references: UNIPARC:UPI000017C687; EMBL:X56974

Query Match 84.5%; Score 49; DB 2; Length 185;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGRWCG 8

|||||||

Db 178 GGGRWCG 184

Search completed: May 23, 2006, 20:31:46
Job time : 40 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2006, 20:43:24 ; Search time 9 Seconds
(without alignments)
1.899 Million cell updates/sec

Title: US-10-674-516B-1
Perfect score: 58
Sequence: 1 CGGGRWCG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	36	62.1		501	6	US-10-505-928-121	Sequence 121, App
2	35	60.3		10	6	US-10-516-079-47	Sequence 47, Appl
3	35	60.3		35	6	US-10-516-079-25	Sequence 25, Appl
4	34	58.6		432	6	US-10-196-749-74	Sequence 74, Appl
5	33	56.9		1300	6	US-10-196-749-269	Sequence 269, App
6	33	56.9		1435	6	US-10-196-749-581	Sequence 581, App
7	33	56.9		4440	6	US-10-196-749-525	Sequence 525, App
8	33	56.9		4590	6	US-10-505-928-569	Sequence 569, App
9	32	55.2		306	7	US-11-181-115-31	Sequence 31, Appl

10	32	55.2	306	7	US-11-181-115-47	Sequence 47, Appl
11	32	55.2	414	6	US-10-532-868-4	Sequence 4, Appli
12	32	55.2	495	6	US-10-511-814-5	Sequence 5, Appli
13	32	55.2	1894	6	US-10-196-749-97	Sequence 97, Appl
14	32	55.2	5738	6	US-10-505-928-150	Sequence 150, App
15	31	53.4	198	6	US-10-196-749-502	Sequence 502, App
16	31	53.4	409	6	US-10-505-928-31	Sequence 31, Appl
17	31	53.4	529	6	US-10-505-928-815	Sequence 815, App
18	31	53.4	671	7	US-11-315-766-30	Sequence 30, Appl
19	31	53.4	4373	7	US-11-118-524-2	Sequence 2, Appli
20	30	51.7	10	7	US-11-257-498-56	Sequence 56, Appl
21	30	51.7	10	7	US-11-140-487A-2071	Sequence 2071, Ap
22	30	51.7	16	7	US-11-264-509A-60	Sequence 60, Appl
23	30	51.7	18	7	US-11-318-939-17	Sequence 17, Appl
24	30	51.7	127	6	US-10-542-038-21	Sequence 21, Appl
25	30	51.7	146	6	US-10-542-038-12	Sequence 12, Appl
26	30	51.7	193	6	US-10-505-928-215	Sequence 215, App
27	30	51.7	238	6	US-10-505-928-559	Sequence 559, App
28	30	51.7	283	6	US-10-196-749-272	Sequence 272, App
29	30	51.7	363	7	US-11-264-509A-2	Sequence 2, Appli
30	30	51.7	676	7	US-11-315-766-20	Sequence 20, Appl
31	30	51.7	691	7	US-11-315-766-22	Sequence 22, Appl
32	30	51.7	720	6	US-10-505-928-383	Sequence 383, App
33	30	51.7	791	7	US-11-318-939-6	Sequence 6, Appli
34	30	51.7	798	6	US-10-511-937-2451	Sequence 2451, Ap
35	30	51.7	810	7	US-11-318-939-11	Sequence 11, Appl
36	30	51.7	1115	6	US-10-196-749-440	Sequence 440, App
37	30	51.7	3010	7	US-11-140-487A-769	Sequence 769, App
38	30	51.7	3010	7	US-11-140-487A-770	Sequence 770, App
39	30	51.7	3011	7	US-11-140-487A-771	Sequence 771, App
40	30	51.7	3020	7	US-11-140-487A-772	Sequence 772, App
41	29	50.0	246	6	US-10-196-749-600	Sequence 600, App
42	29	50.0	340	6	US-10-505-928-373	Sequence 373, App
43	29	50.0	449	7	US-11-322-245-1	Sequence 1, Appli
44	29	50.0	1141	6	US-10-196-749-120	Sequence 120, App
45	29	50.0	1170	6	US-10-511-937-3007	Sequence 3007, Ap

ALIGNMENTS

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RESULT 1
US-10-505-928-121
; Sequence 121, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 121
; LENGTH: 501

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-121

Query Match 62.1%; Score 36; DB 6; Length 501;
Best Local Similarity 83.3%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGGRW 6
||| |
Db 370 CGGGPW 375

RESULT 2

US-10-516-079-47
; Sequence 47, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; APPLICANT: GONDA, Matthew A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-WO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/384,171
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Pep8-NJ0361 sequence
US-10-516-079-47

Query Match 60.3%; Score 35; DB 6; Length 10;
Best Local Similarity 71.4%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGGRWC 7
||| |
Db 1 CGGGKKC 7

Search completed: May 23, 2006, 20:46:33
Job time : 10 secs

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2006, 20:43:05 ; Search time 181 Seconds
 (without alignments)
 20.474 Million cell updates/sec

Title: US-10-674-516B-1
 Perfect score: 58
 Sequence: 1 CGGGRWCG 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_Main:*
 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	58	100.0	8	5	US-10-674-516-1	Sequence 1, Appli
2	49	84.5	225	4	US-10-437-963-106003	Sequence 106003,
3	49	84.5	302	6	US-11-096-568A-25943	Sequence 25943, A
4	48	82.8	308	4	US-10-437-963-156549	Sequence 156549,
5	46	79.3	114	4	US-10-437-963-108422	Sequence 108422,
6	46	79.3	427	6	US-11-172-740-333	Sequence 333, App
7	45	77.6	83	4	US-10-437-963-161633	Sequence 161633,
8	45	77.6	117	4	US-10-437-963-120602	Sequence 120602,
9	45	77.6	269	4	US-10-705-791-9	Sequence 9, Appli
10	45	77.6	416	4	US-10-437-963-164329	Sequence 164329,
11	44	75.9	59	4	US-10-437-963-113259	Sequence 113259,

12	44	75.9	884	5	US-10-450-763-39518	Sequence 39518, A
13	43.5	75.0	169	4	US-10-425-114-42832	Sequence 42832, A
14	43	74.1	83	4	US-10-437-963-112746	Sequence 112746,
15	43	74.1	84	4	US-10-425-115-255866	Sequence 255866,
16	43	74.1	96	4	US-10-767-701-56720	Sequence 56720, A
17	43	74.1	97	4	US-10-425-114-48971	Sequence 48971, A
18	43	74.1	100	4	US-10-425-115-361421	Sequence 361421,
19	43	74.1	103	4	US-10-437-963-186614	Sequence 186614,
20	43	74.1	113	4	US-10-425-115-284781	Sequence 284781,
21	43	74.1	116	4	US-10-425-115-188129	Sequence 188129,
22	43	74.1	136	4	US-10-437-963-203306	Sequence 203306,
23	43	74.1	203	4	US-10-437-963-120411	Sequence 120411,
24	43	74.1	203	5	US-10-450-763-42036	Sequence 42036, A
25	43	74.1	207	5	US-10-450-763-36595	Sequence 36595, A
26	43	74.1	262	6	US-11-097-143-22041	Sequence 22041, A
27	43	74.1	305	4	US-10-437-963-122157	Sequence 122157,
28	43	74.1	500	5	US-10-784-004-396	Sequence 396, App
29	43	74.1	501	4	US-10-316-253-18	Sequence 18, Appl
30	43	74.1	533	6	US-11-087-099-5854	Sequence 5854, Ap
31	43	74.1	539	4	US-10-437-963-172380	Sequence 172380,
32	43	74.1	561	5	US-10-618-281-47	Sequence 47, Appl
33	43	74.1	623	4	US-10-437-963-148905	Sequence 148905,
34	43	74.1	2338	4	US-10-029-386-31982	Sequence 31982, A
35	43	74.1	19725	4	US-10-084-846A-4	Sequence 4, Appli
36	42	72.4	175	4	US-10-425-115-266440	Sequence 266440,
37	42	72.4	188	6	US-11-087-099-8568	Sequence 8568, Ap
38	42	72.4	188	6	US-11-188-298-17509	Sequence 17509, A
39	42	72.4	201	4	US-10-767-701-57762	Sequence 57762, A
40	42	72.4	229	4	US-10-437-963-160205	Sequence 160205,
41	42	72.4	372	4	US-10-425-115-351284	Sequence 351284,
42	42	72.4	411	4	US-10-425-114-67026	Sequence 67026, A
43	42	72.4	709	4	US-10-437-963-174410	Sequence 174410,
44	42	72.4	1078	4	US-10-425-115-293711	Sequence 293711,
45	41	70.7	22	6	US-11-111-953-579	Sequence 579, App

ALIGNMENTS

RESULT 1

US-10-674-516-1

; Sequence 1, Application US/10674516

; Publication No. US20050187162A1

; GENERAL INFORMATION:

; APPLICANT: Dhanaraj, Sridevi

; APPLICANT: Gosiewska, Anna

; APPLICANT: Rezania, Ali

; APPLICANT: Heavner, George A.

; APPLICANT: Lin, Xuanhan

; APPLICANT: Yi, Chin-Feng

; TITLE OF INVENTION: Novel Peptide with Osteogenic Activity

; FILE REFERENCE: 1264-15

; CURRENT APPLICATION NUMBER: US/10/674,516

; CURRENT FILING DATE: 2003-09-30

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized primer
US-10-674-516-1

Query Match 100.0%; Score 58; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGRWCG 8
|||
Db 1 CGGGRWCG 8

RESULT 2

US-10-437-963-106003
; Sequence 106003, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106003
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10488C.1.pep
US-10-437-963-106003

Query Match 84.5%; Score 49; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGRWCG 8
|||
Db 22 GGGRWCG 28

Search completed: May 23, 2006, 20:46:19
Job time : 182 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 23, 2006, 20:31:19 ; Search time 50 Seconds
 (without alignments)
 14.005 Million cell updates/sec

Title: US-10-674-516B-1
 Perfect score: 58
 Sequence: 1 CGGGRWCG 8

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	43	74.1		296	2	US-09-252-991A-17538	Sequence 17538, A
2	43	74.1		447	2	US-09-949-016-6956	Sequence 6956, Ap
3	43	74.1		563	2	US-09-949-016-6955	Sequence 6955, Ap
4	43	74.1		620	2	US-09-949-016-7495	Sequence 7495, Ap
5	43	74.1		620	2	US-09-949-016-7496	Sequence 7496, Ap
6	43	74.1		620	2	US-09-949-016-7497	Sequence 7497, Ap
7	43	74.1		620	2	US-09-949-016-7498	Sequence 7498, Ap
8	42	72.4		269	2	US-09-252-991A-29509	Sequence 29509, A
9	41	70.7		551	2	US-09-130-491-16	Sequence 16, Appl
10	41	70.7		608	2	US-09-130-491-13	Sequence 13, Appl

11	41	70.7	727	2	US-09-445-023A-1	Sequence 1, Appli
12	41	70.7	727	2	US-09-445-023A-12	Sequence 12, Appl
13	41	70.7	949	2	US-09-568-559-2	Sequence 2, Appli
14	41	70.7	950	2	US-09-321-987B-4	Sequence 4, Appli
15	41	70.7	967	2	US-09-130-491-2	Sequence 2, Appli
16	40.5	69.8	75	2	US-09-621-976-5341	Sequence 5341, Ap
17	39	67.2	70	2	US-09-248-796A-21926	Sequence 21926, A
18	39	67.2	147	2	US-09-134-001C-2854	Sequence 2854, Ap
19	39	67.2	439	2	US-09-902-540-13020	Sequence 13020, A
20	39	67.2	2616	2	US-09-303-518D-879	Sequence 879, App
21	39	67.2	3854	2	US-09-949-016-7876	Sequence 7876, Ap
22	38	65.5	120	2	US-09-252-991A-24786	Sequence 24786, A
23	38	65.5	122	1	US-07-734-534A-1	Sequence 1, Appli
24	38	65.5	208	2	US-09-252-991A-25609	Sequence 25609, A
25	38	65.5	352	2	US-09-902-540-9796	Sequence 9796, Ap
26	38	65.5	416	2	US-09-540-236-2215	Sequence 2215, Ap
27	38	65.5	635	2	US-09-270-767-44609	Sequence 44609, A
28	38	65.5	1152	2	US-09-303-518D-195	Sequence 195, App
29	38	65.5	2088	2	US-09-548-372D-13	Sequence 13, Appl
30	38	65.5	2088	2	US-09-548-367D-13	Sequence 13, Appl
31	38	65.5	2088	2	US-09-551-853D-13	Sequence 13, Appl
32	38	65.5	2088	2	US-09-548-376D-13	Sequence 13, Appl
33	38	65.5	2088	2	US-09-548-373D-13	Sequence 13, Appl
34	38	65.5	2088	2	US-09-548-366F-13	Sequence 13, Appl
35	38	65.5	2088	2	US-09-548-368D-13	Sequence 13, Appl
36	38	65.5	2508	2	US-09-627-650B-7	Sequence 7, Appli
37	38	65.5	2508	2	US-09-436-063C-7	Sequence 7, Appli
38	38	65.5	2544	2	US-09-627-650B-3	Sequence 3, Appli
39	38	65.5	2544	2	US-09-436-063C-3	Sequence 3, Appli
40	38	65.5	2601	2	US-09-627-650B-9	Sequence 9, Appli
41	38	65.5	2601	2	US-09-436-063C-9	Sequence 9, Appli
42	38	65.5	2732	2	US-09-086-436-30	Sequence 30, Appl
43	37.5	64.7	113	2	US-09-252-991A-29076	Sequence 29076, A
44	37	63.8	9	1	US-08-462-661A-110	Sequence 110, App
45	37	63.8	9	7	5318899-76	Patent No. 5318899

ALIGNMENTS

```

RESULT 1
US-09-252-991A-17538
; Sequence 17538, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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; SEQ ID NO 17538
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17538

Query Match 74.1%; Score 43; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGGRWC 7
|||
Db 70 GGGRWC 75

Search completed: May 23, 2006, 20:32:41
Job time : 51 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 23, 2006, 20:22:34 ; Search time 195 Seconds
(without alignments)
18.758 Million cell updates/sec

Title: US-10-674-516B-1
Perfect score: 58
Sequence: 1 CGGGRWCG 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	58	100.0	8	9	ADZ25704	Adz25704 Peptide u
2	49	84.5	85	4	AAU42392	Aau42392 Propionib
3	49	84.5	85	6	ABM38911	Abm38911 Propionib
4	46	79.3	427	10	AEF28133	Aef28133 Lead_Cere
5	45	77.6	269	3	AAV71010	Aay71010 Chicken p
6	45	77.6	432	1	AAP92149	Aap92149 Large env
7	45	77.6	432	1	AAP92148	Aap92148 Large env

8	45	77.6	662	2	AAW68401	Aaw68401	FeLV-B en
9	44	75.9	108	4	AAU65014	Aau65014	Propionib
10	44	75.9	108	6	ABM61533	Abm61533	Propionib
11	44	75.9	884	4	ABG09159	Abg09159	Novel hum
12	43.5	75.0	169	8	ADX73466	Adx73466	Plant ful
13	43	74.1	97	8	ADX79605	Adx79605	Plant ful
14	43	74.1	203	4	ABG11677	Abg11677	Novel hum
15	43	74.1	207	4	ABG06236	Abg06236	Novel hum
16	43	74.1	258	9	ADY20186	Ady20186	PRO polyp
17	43	74.1	262	4	ABB65083	Abb65083	Drosophil
18	43	74.1	296	7	ABO68792	Abo68792	Pseudomon
19	43	74.1	500	7	ADD47142	Add47142	Rat Prote
20	43	74.1	500	7	ADD47146	Add47146	Rat Prote
21	43	74.1	500	9	AEC12050	Aec12050	Rat surro
22	43	74.1	501	7	ADF30455	Adf30455	Rat angio
23	43	74.1	501	9	AEA29108	Aea29108	Mus muscu
24	43	74.1	559	8	ABM84024	Abm84024	Human dia
25	43	74.1	561	8	ADU24099	Adu24099	Human asp
26	43	74.1	606	5	ABP52121	Abp52121	Homo sapi
27	43	74.1	620	7	ADE10036	Ade10036	Novel pro
28	43	74.1	2338	8	ABO58348	Abo58348	Human gen
29	43	74.1	2367	4	AAU31850	Aau31850	Novel hum
30	43	74.1	19938	6	ABP76678	Abp76678	Streptomy
31	42	72.4	151	4	AAU45804	Aau45804	Propionib
32	42	72.4	151	6	ABM42323	Abm42323	Propionib
33	42	72.4	269	7	ABO80763	Abo80763	Pseudomon
34	42	72.4	411	8	ADY11211	Ady11211	Plant ful
35	41	70.7	32	8	ADK01482	Adk01482	Hepatitis
36	41	70.7	109	6	ABU70643	Abu70643	Human adi
37	41	70.7	180	4	AAB95532	Aab95532	Human pro
38	41	70.7	543	7	ABM88929	Abm88929	Rice abio
39	41	70.7	727	2	AAW78435	Aaw78435	Human ADA
40	41	70.7	896	3	AAB21265	Aab21265	Mouse met
41	41	70.7	949	7	ADG72483	Adg72483	Human agg
42	41	70.7	949	9	ADZ21014	Adz21014	Human agg
43	41	70.7	950	2	AAAY49501	Aay49501	Human MET
44	41	70.7	950	3	AAAY53899	Aay53899	Amino aci
45	41	70.7	950	4	AAB73549	Aab73549	Human ADA

ALIGNMENTS

RESULT 1

ADZ25704

ID ADZ25704 standard; peptide; 8 AA.

XX

AC ADZ25704;

XX

DT 30-JUN-2005 (first entry)

XX

DE Peptide useful in an osteoinductive composition.

XX

KW osteoblast; cell proliferation; bone fracture; rheumatoid arthritis;

KW osteoporosis; cell differentiation; osteopathic; antiarthritic;

KW antirheumatic.

XX

OS Synthetic.
 XX
 PN WO2005032461-A2.
 XX
 PD 14-APR-2005.
 XX
 PF 10-SEP-2004; 2004WO-US029649.
 XX
 PR 30-SEP-2003; 2003US-00674516.
 XX
 PA (ETHI) ETHICON INC.
 XX
 PI Dhanaraj S, Gosiewska A, Rezania A, Heavner GA, Lin X, Yi C;
 XX
 DR WPI; 2005-315317/32.
 XX
 PT Composition useful for promoting proliferation of osteoblasts and
 PT treating bone fractures comprises an isolated recombinant peptide
 PT component having specific sequence.
 XX
 PS Claim 59; SEQ ID NO 1; 47pp; English.
 XX
 CC The invention relates to an osteoinductive composition comprising an
 CC isolated recombinant peptide component, its derivative or salt. Also
 CC described are: (i) an osteoinductive implant comprising a bone-compatible
 CC matrix and a recombinant peptide associated with the bone-compatible
 CC matrix; (ii) a method of preparing an osteoinductive composition
 CC involving combining the bone-compatible matrix with a recombinant
 CC peptide, and immobilizing the recombinant peptide to or within the bone-
 CC compatible matrix; (iii) a composition comprising the reaction product of
 CC the bone-compatible matrix, osteoinductive cells and a recombinant
 CC peptide; (iv) a kit including at least one container comprising a
 CC recombinant peptide and a material selected from bone-compatible matrix,
 CC carrier or aqueous solvent, stabilizer, preservative, thickener,
 CC solubilizer, and cells capable of forming bone; (v) a method of promoting
 CC proliferation of osteoblasts involving administering the osteoinductive
 CC composition; (vi) a method of promoting the proliferation and/or
 CC differentiation of mesenchymal stem cells involving combining the stem
 CC cells ex vivo or in vivo with the osteoinductive composition; (vii) an
 CC isolated or recombinant peptide having a sequence given as SEQ ID No:1 in
 CC the specification; and (viii) an isolated DNA sequence encoding the
 CC peptide of SEQ ID No:1. The composition of the invention is useful for
 CC promoting proliferation of osteoblasts, treating bone fractures, treating
 CC disease (e.g. rheumatoid arthritis and osteoporosis) or anomalies
 CC associated with deficient sites of bone (e.g. craniofacial anomalies,
 CC dental anomalies and periodontal anomalies). The bone-compatible matrix
 CC provides slow release of the peptide component and/or a structure for
 CC developing bone in a patient. The composition provides a permissive
 CC matrix structure for deposition of bone-forming cells or cause growth
 CC stimulation of bone-forming cells or induces the differentiation of
 CC appropriate progenitors of bone-forming cells. This sequence represents a
 CC peptide useful in the composition of the invention.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 58; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CGGGRWCG 8
        |||||
Db      1 CGGGRWCG 8
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RESULT 2

AAU42392

ID AAU42392 standard; protein; 85 AA.

XX

AC AAU42392;

XX

DT 27-FEB-2002 (first entry)

XX

DE Propionibacterium acnes immunogenic protein #3288.

XX

KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.

XX

OS Propionibacterium acnes.

XX

PN WO200181581-A2.

XX

PD 01-NOV-2001.

XX

PF 20-APR-2001; 2001WO-US012865.

XX

PR 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX

DR WPI; 2001-616774/71.

DR N-PSDB; AAS59517.

XX

PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.

XX

PS Example 1; SEQ ID NO 3587; 1069pp; English.

XX

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

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SQ Sequence 85 AA;

Query Match 84.5%; Score 49; DB 4; Length 85;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGRWCG 8
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Db 15 CGYGRWCG 22

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